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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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AG156412 Pan trog1
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AV755654 AV755654
AG046383 Pan trog1
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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION KEYWORDS LOCUS DEFINITION RESULT 1 AA515728/c FEATURES COMMENT JOURNAL source AA515728
439 bp mRNA linear EST 19-AUG-1997 mg70f04.51 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940159 similar to contains Alu repetitive element; contains element PTR5 repetitive element; mRNA sequence.

AA515728 cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 634 Std Error: 0.00
Seq primer: -40ml3 fwd. Erf from Amersham
High quality sequence stop: 358.
Location/Qualifiers Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Me
Emmert-Buck, M.D., Ph.D. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 439) Tumor Gene Index Unpublished (1997) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Homo sapiens AA515728.1 human. /tissue_type="liposarcoma" /lab_host="DH10B" /clone="IMAGE:940159" /clone_lib="NCI_CGAP_Lip2" /organism="Homo sapiens" /db_xref="taxon:9606" GI:2255328 Jeffrey Medeiros, M.D., pamp10; mRNA made from liposarcoma, Hominidae; Michael

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REFERENCE
AUTHORS
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                                                        Clones are available from Research Genetics (info@resgen.com). BA end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                              Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B65075 461 bp CIT-HSP-2015M9.TFB CIT-HSP Homo
                                                                                                                                       Email: mdadams@tigr.org
                                                                                                                                                                                                                                                Other_GSSs: CIT-HSP-2015M9.TRB
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        Location/Qualifiers
/organism="Homo sapiens"
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Suh, E., Wible, C., Shizuya, H.,
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                                                                                                    Unpublished (1997)
Other_GSSs: RPCI-I1-203E3.TJ
Other_GSSs: RPCI-I1-203E3.TJ
Contact: Shaying Zhao, William Nier
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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                Email: hbe@ttigr.org
Clones are derived from the human BAC library RPCI-11. For library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased f BACPAC Resources (http://bacpac.med.buffalo.edu/ordering)
Research Genet cs (library //bacpac.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                    DNA sequence.
AQ415030
AQ415030.1 G1
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
                                                                                                                                                                                                                Map Building
                                                                                                                                                                                                                               Use of BAC End Sequences
                                                                                                                                                                                                                                                        Zhao,S.,
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 711)
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RPCI-11-203E3.TV
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a 118 (
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/clone="2015M9"
/clone_lib="CIT-HSP"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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86.2%;
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Primates;
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Pred. No. 4.3e-26;
0; Mismatches 44;
                                                                                                                                                                         William Nierman,
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Rockville,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%;
al Similarity 85.1%;
275; Conserva+:--
                                                    Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, Germ Research Center (DKFZ); Email s.wiemann@dKfz-heidelbe sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium
                                                                                                                                                  Blum, H., Bauersachs, S.,
EST (Blum, et al.)
Unpublished (1999)
Contact: Blum H
                                                                                                                                                                                                                                                                                                    DKFZp434H1730_r1 434 (synonym: )
DKFZp434H1730 5', mRNA sequence.
AL079734
No s1 sequence available. This clone (DKFZp434H1730) is available at Please contact the RZPD: Ressourcenzentrum,
                                          Munich/Germany) within 
Genome Project.
                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 386)
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                                                                                                                                                                                                                                              Homo sapiens
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/SEX="Male"
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/Cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/**RPCIII Human Male BAC Library"
/**150 c 141 g 150 t
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/clone="RPCI-11-203E3"
/clone_lib="RPCI-11"
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/db_xref="GDB:7577666"
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Primates;
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Pred. No. 7.8e-26;
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Best Local Similarity
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                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                          AUTHORS
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                                                                        Contact: Shaying Zhao, William Niern Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased 1
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering)
                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 639)
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RPCI11-160D20.TV
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                   Homo sapiens
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/clone_lib="434 (synonym: htes3)"
/tissue_type="restits"
/dev_stage="adult"
/lab_host="pH10B"
/note="Vector: pSport1; Site_1: Not: a 75 c 94 g 89 t
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/db_xref="taxon:9606"
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Pred. No. 1.8e-25;
0; Mismatches 56
                                                                                                                                                  William Nierman,
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                                                                                                                                                   Mark Adams
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yaqa, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa
                                                                                                                                                                                                                                          AG183410 1 GI:16713090
AG183410.1 GI:16713090
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA,
Male BAC Library clone:RP43-056004.TJ.
                                                                                                                                                        Fujiyama, A., Hattori, M., Totoki, Y., Watanabe, H. a
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                           Unpublished
                                                                                                                                                                                                                                     Pan troglodytes
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Class:
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                                                                                                                                       end sequences of Library RPCI-43
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/note="Vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
1 148 c 129 g 209 t
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/db_xref="GDB:7561147"
/db_xref="taxon:9606"
/clone="RPCI-11-160D20"
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Pred. No. 1.6e-25;
0; Mismatches 58;
                                                                                                                                                        and Sakaki, Y
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RP43-056004.TJ,
                                                                                                                                                                     Taylor, T.D.,
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COMMENT

Unpublished (1997) Other_GSSs: 345H13.TPB Contact: Mark Adams

TITLE JOURNAL

Building

Use of a random BAC

End

Sequence Database

for

Sequence-Ready

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KEYWORDS
SOURCE
ORGANISM
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274;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 642) Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linh, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya and Venter, J.C.
                                                                                                                                                        sequence.
B59854
                                                                                                                         GSS
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CIT-HSP-345H13.TVB CIT-HSP Homo
                                                                                          Homo sapiens
                                                                                                                                         B59854.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee
/clone_lib="RPCI-43 Chimpanzee
148 c 166 g 154 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-056004.TJ"
                                                                                                                                       GI:2614572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
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Pred. No. 4.4e-25;
0; Mismatches 55;
             Field, C.E., Bass, S., Linher, K., Suh, E., Wible, C., Shizuya, H., S
                                                                                                                                                                                                                                                                                                  2054
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                                                                                                                                                                               sapiens
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                                                                        Euteleostomi;
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Homo sapiens, interleukin 10,
BC022315
BC022315.1 GI:18490360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0208 Fax: 301 838 0208 Email: mdadams@tigr.org
Direct Submission
Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MCC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                     Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are available from
                                                                     Strausberg, R.
                                                                                                                                       Homo sapiens
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mmalia; Eutheria; Primates;
(bases 1 to 1655)
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/db_xref="GDB:5363319"
/db_xref="taxon:9606"
/clone="345H13"
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Pred. No. 4.8e-25;
D; Mismatches 52;
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IMAGE:4691490,
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8 Ъ Q 밁 δÃ 밁 οy ģ Ş 밁 Q

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POCUS.

Eukaryota;

Metazoa; Chordata; Craniata;

Vertebrata;

Euteleostomi;

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RESULT
BG927980
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Best Local S
Matches 269
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                                                                                                                                                                                                                                                                                                                                                                                            269;
                               sequence.
BG927980
BG927980.1
EST.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1083514
This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                             HNC45-1-G7.R HNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Homo sapiens
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                  human.
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/tissue_type="Lung"
/clone_lib="NIH_MGC_77"
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/db_xref="LocusID:3586"
/db_xref="taxon:9606"
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376 c 363 g 43
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84.9%;
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Pred. No. 3.8e-25;
0; Mismatches 48
                                                                                             Normal
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RESULT 1
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                                                                                AW970571.1
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 521)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R.
                                                                                                       AW970571 52:
EST382652 MAGE resequences,
AW970571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequenced tags osteoarthritic osteoarthritis osteoarthritis (21482651
                                                                    human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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610-270-5598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HNC (Human Normal Cart.
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/note="Vector: psPorT I; Site_1: Si
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Pred. No. 6.5e-25;
0; Mismatches 47;
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  Gaspard, R.,
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                            Euteleostomi;
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          2 (bases 1 to 669)
Fujiyama, A., Hattor
                                                Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
                                                                                                                          sequence.
AG156412.1 GI:16686090
AG156412.1 GI:16686090
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA,
Male BAC Library clone:RP43-021A10.TJ.
Pan troglodytes
                                                             Fujiyama, A., Hattori, M.,
Totoki, Y., Watanabe, H. a
                                   Unpublished
                                                                                                               Eukaryota;
                                                                                                                                                                                                                     Pan troglodytes DNA,
                                                                                                                                                                                                                                  AG156412
                                                                                                     Mammalia; Eutheria;
                                                                                        (sites)
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Watanabe, H.

and

Toyoda,A., nd Sakaki,Y

Taylor, T.D.,

Hattori, M.,

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sutheria; Primates; Catarrhini; Hominidae; Pan.

clone_lib:RPCI-43 Chimpanzee

Taylor, T.D.,

669 bp DNA clone: RP43-021A10.TJ,

linear

genomic

survey

GSS 09-JAN-2002

669

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1783 cgagatgggcgtatcccctgaggtcaggagtttgtgaccagcctggccaacatggtgaaa 1842
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                                                                                                      agctgagatcgtgccgttgcactccagcctcagcaacagagcgagactccatctcaaaaa
                                                                                                                                                               AGCAACTCGGGAGGCTGAGGCAGGAGAATCACTTGAGCCCAGGAGGCAGAGCTTGCAGTG
                                                                                                                                                                                  agctacttggggaagctgaggcaagagaatcgcttgaacccaggagaccggaagttgcagtg
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Quackenbush, J.
Quackenbush, J.
Assessment of gene expression patterns in a model
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: Forward.
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Plate: 279
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: 301 838 3528
: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens" .
/db_xref="taxon:9606" .
/db_xref="taxon:9606" .
/clone_lib="MAGE resequences, .
/note="Vector: pBluescriptSKm" .
128 c 141 g 89 t
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82.5%;
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Pred. No. 8.8e-25;
0; Mismatches 58
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JOURNAL
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Best Local :
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9110)
Clones are derived from the chimpanzee BAC library RPCI.43 This BAC
                                                                                                                                                                                                                                                             AQ746057 897 bp
HS_2277_A2_G10_T7C CIT Approved is
HS_2677_C10_T7C CIT Approved is
HS_2677_A2_G10_T7C CIT Approved is
HS_267_A2_G10_T7C CIT Approved is
HS_26
                                                                                                                 Mammalia; Eutheria;
1 (bases 1 to 897)
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                                                                                                                                                                                                      Homo sapiens
Sequence-tagged
                                                   Mahairas,G.G., Waliace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                 Hood, L
                                                                                                                                                                           Eukaryota;
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
168 c 122 g 242 t
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/db_xref="taxon:9598"
/clo="RP43-021A10.TJ"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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83.6%;
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Pred. No. 7.9e-25;
0; Mismatches 53
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   sequence
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approach to
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mapping
                                                       Holzman, T., Adams, M.D. and
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Best Local Similarity
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                    AUTHORS
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2277 row: M column: 20
Seq primer: T7
Class: BAC ends
                                                                                                                                                          AW020150
df05a09.y1 Morton Fetal Cochlea
IMAGE:2482456 5', mRNA sequence.
AW020150
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 397) Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A and Morton, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 897.
Location/Qualifiers
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                                                                                      Homo sapiens
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174 c 177 g 218 t 21 others
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/db_xref="taxon:9606"
/clone="plate=2277 Col=20 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                              GI:5873680
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                                                                                                                                                                                               Homo sapiens
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                      Bieber, F.R.
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AQ627870 614 CITBI-E1-2657J22.TR CITBI-E1 DNA sequence.
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This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Plate: LLAM617 row: A column: 17
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75 Francis Street, Harvard Medical School,
Tel: 617 732 7980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Morton, C. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ccmorton@bics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation of novel and known genes from a human fetal cochlear cDN library using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
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Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org
Clones are available from Research
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Fax: 301 838 0208
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The Institute for Genomic Research
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Use of BAC End Sequences from CalTech Libraries for Sequence-Rea
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Mammalia; Eutheria;
1 (bases 1 to 614)
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/note="Vector: pBeloBAC11;
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Best Local Similarity 83.6%;
Matches 270; Conservative
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Contact: Zeguang Han Chinese National Human Genome Center at Shanghai Sil Guo Shoujing Road, Zhangjiang Hi-Tech Park, F 201203, P. R. China Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu,J., Zhao,M., Huàng,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zen,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 827)
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AV755654.1 GI:10913502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
1 207 c 202 g 188 t 4 others
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/db_xref="taxon:9606"
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Pred. No. 1e-24;
0; Mismatches 53;
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Search completed: September 27, 2002, 14:55:35 Job time: 10047 sec

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Result
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Maximum DB seq length: 200000000
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-482-293A-1
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US-08-485-618-98
US-08-485-618-98
US-08-485-618-97
US-08-482-293A-98
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US-08-605-672-96
US-08-482-293A-96
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ALIGNMENTS	US-08-395-800A-7 US-09-608-285A-8 US-09-608-285A-59 US-09-608-285A-59 US-09-608-285A-59 US-09-167-681-45 US-09-167-681-81 US-09-323-06251-81 US-09-323-06251-81 US-09-323-873A-6 US-09-323-873A-6 US-09-38-982-358 US-08-467-254-5 US-08-499-927-5 PCT-US94-08806-28 PCT-US94-08806-28 PCT-US95-16626-5 PCT-US95-16626-5 PCT-US95-16626-5	
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RESULT 1 US-08-485-618-96 STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois COUNTRY: United States ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: Patent No. APPLICATION NUMBER: US 08/173,497 FILING DATE: 23-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/286,889 FILING DATE: 5-AUG-1994 PRIOR APPLICATION DATA: APPLICATION UMBER: US 08/362,652 FILING DATE: 21-DEC-1994 ATTORNEY/AGENT INFORMATION: NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,559 REGISTRATION NUMBER: 38,559 REGISTRATION NUMBER: 27866/3279. INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: CORRESPONDENCE ADDRESS: CORRESPONDENCE Marshall, O'Toole, Gerstein, Murray & Borun ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun APPLICANT: Gallatin, W. Michael APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5728533el TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 PRIOR APPLICATION DATA: NUMBER OF SEQUENCES: TELEFAX: 25-3856 FILING DATE: CLASSIFICATION: TELEPHONE: APPLICATION NUMBER: US/08/485,618 6, Application 5728533 312-474-0448 US/08485618 103 27866/32797 Human 2 Integrin Alpha Subunit

Appl

; TOPOLOGY: li ; MOLECULE TYPE: US-08-485-618-96

SEQUENCE CHARACTERISTICS:

LENGTH: 2499 base pairs TYPE: nucleic acid

STRANDEDNESS:

linear single

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US-08-605-672-96
; Sequence 96, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el
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Best Local Sim
Matches 411;
                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                     CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                             ADDRESSEE: Marshall, O'T
STREET: 233 South Wacker
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60605-5402
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FILING DATE:
CLASSIFICATION:
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Similarity 72.6%;
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Pred. No. 2.7e-44;
0; Mismatches 13;
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Best Local :
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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LENGTH: 2499 base pairs
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APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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                                                            CCAGCCCGAGCCAGCAGCCTGGTGGATCCCATCGTCCAACTGAAAGGCCTGACGTTCA
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72.6%;
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Pred. No. 2.7e-44;
0; Mismatches 13
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RESULT 3 US-08-482-293A-96

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Best Local Similarity
Matches 411; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 249 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                    2773
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2833
                                                                                                                                                                                                                                                                                  2713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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APPLICATION NUMBER: US 0
FILING DATE: 23-DEC-1993
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MEDIUM TYPE: Floppy disk
                                                                                             2893
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, G
STREET: 233 South Wacker Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                ggcccccgcagtgcatctccgattcctccccattcccccacagagtgtccc.catcaagag
                                                                                                                                         ccagacagtccccgacgccacgccaggtaggtccctggcaggagctgcageagggggttg
                                                                                                                                                                                                    tggggagaactcatactcaaagggttcctgcctgcttgggctcgcgcgctcggagatcat 2832
                                                                                                                          CCAGACAGTCCCCGACGCCACGC-----
                                                                                                                                                                                      TGGGGAGAACTCATACTCAAAGGGTTCCTGCCTCCTGCTGGGCTCGCGCTGGGAGATCAT: 401
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e, 6300 Sear Tower
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                                                              -CAGAGTGTCCACATCAAGAG
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RESULT 4
US-08-943-363-96
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                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3268
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606-6402
COMPUTER READABLE FORM:
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APPLICANT: Van der Vieren, Monica
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                                                                                            SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 233 Sc
CITY: Chicago
                  STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                    TELEFAX:
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                                                                                                                                                    TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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233 South Wacker Drive, 6300 Sear Tower
                                      single
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
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US-09-193-043-96
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LENGTH: 2499
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No. 6251395
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Best Local
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                                                     SOFTWARE: PatentIn Ver.
TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 2.7e-44;
0; Mismatches 13
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RESULT 6
US-08-173-497-1
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Best Local Similarity 72.6
Matches 411; Conservative
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                    ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                    APPLICANT: Gallatin, W. Michael APPLICANT: Van Der Vieren, Monica TITLE OF INVENTION: No. 5437958el TITLE OF INVENTION: Subunit
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 ATTORNEY/AGENT
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            CLASSIFICATION:
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                          FILING DATE:
                                      APPLICATION NUMBER:
                                                                                                                                                                        CITY: Chicago
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                                                                                                                                                          Illinois
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233 S. Wacker Drive, (
INFORMATION
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Pred. No. 2.7e-44;
0; Mismatches 13
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6300 Sears
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NUMBER OF SEQUENCES:

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                                   Sequence 1, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
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Best Local Similarity
Matches 411; Conserv
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
APPLICANT: Gallatin, W. Mich APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5470953el
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TELEFAX: 312-474-0448
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Pred. No. 3.1e-44;
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; LOCATION:
US-08-286-889-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.3%;
Best Local Similarity 72.6%;
Matches 411; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 TELEFAX: 312-474-0448
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                              2893
                                                                                                                                                                                                                                                                                                                                                             2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 2786
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                             281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 233 Sc
CITY: Chicago
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                           actgggcaaacaatagtaacaggcactgagccctgggccctccccactggcctttgcagt 3132
                                                                                                                                                                                                                                                              CCAGACAGTCCCCGACGCCACGC------
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Pred. No. 3.1e-44;
0; Mismatches 13;
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; LOCATION:
US-08-485-618-1
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 5-LDEC-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 36,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3279:
TELECHONE: 312-474-6300
TELEFAX: 312-474-6300
TELEFAX: 32-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERSTICS:
LENGTH: 3726 base pairs
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                                                              Query Match
Best Local Similarity
                                              Matches 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08485618 Patent No. 5728533
2713 ggactcctggctcacaggcttctgcctccaggcctgtggcccgaccctgcacagagtctg 2772
                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                       MOLECULE TYPE:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                       LENGTH: 3726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                            Conservative
                                                                                                                                                                                                                       CDNA
                                                          7.3%;
72.6%;
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                                            0;
                                          Score 241.2; DB 1;
Pred. No. 3.1e-44;
0; Mismatches 13;
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                                          Indels 142; Gaps
                                                                              Length 3726;
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9362-652-1 ance 1, Application US/08362652 BRAL INFORMATION: PPLICANT: Gallatin, W. Michael PPLICANT: Van der Vieren, Monica ITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit BMBER OF SEQUENCES: 93 BMBER OF SEQUENCES: 93 BADRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois COUNTRY: United States COUNTRY: United States ZIP: 60606-6402 MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 BRENT APPLICATION NUMBER: US/08/362,652 FILING DATE: CLASSIFICATION: 435 LIOR APPLICATION NOATA: APPLICATION NUMBER: US 08/173,497 FILING DATE: 23-DEC-1993 APPLICATION NUMBER: US 08/286,889 FILING APTE: 5-AUG-1994 TONNEY/ACENT INFORMATION: NAME: Williams Jr., Joseph A.	RESULT US-08-362 Sequence Patent APPL APPL ITITLE I	
53 cggccacgggcatcctgacagtggtg 3278 	Qу 32 Db 6	
93 ccagccogagccagcagagcctggtggatcccatcgtccaactgaaaggcctgacgttca 3252 	Qy 31 Db 6	
33 ttgcactgatgcagtactcaaacctcctgaagatccacttcaccttcacccaattccgga 3192 	Qy 31 Db 5	
7GT 558		
Telegraphy Tel	Db 50 Qy 307	
a tygacatcytottcotyattyacygototygaaycattyacoaaaatgacotttaaccag 301	 	
3 ggccccgcagtgcatctccgattcctcccattcc	. 2	
33 ccagacagtccccgacgccacgccaggtaggtccctggcaggagctgcaggagggggttg 2892	Оу 28 Db 4	
73 tggggagaactcatactcaaagggttcctgcctcctgctgggctcgcgctgggagatcat 2832 	Qy 27 Db 3	
	Db 2	

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                                                               Sequence 1, Application US/08605672
Patent No. 5817515
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Best Local
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el
NUMBER OF SEQUENCES: 103
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
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REFERENCE/FOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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LOCATION:
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STRANDEDNESS: single
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Pred. No. 3.1e-44;
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              2 Integrin Alpha Subunit
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; LOCATION:
US-08-605-672-1
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Best Local Similarity 72.6%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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PRIOR APPLICATION DATE:
APPLICATION UNMEER: US 08/362,652
FILING DATE: 21-DEC-1994
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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ADDRESSEE: Marshall, O'To
STREET: 233 South Wacker
                                                                                                                                                           2893
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CURRENT APPLICATION DATA:
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504
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STREET: 233 So
CITY: Chicago
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STRANDEDNESS: single
TOPOLOGY: linear
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             atgaagggctttgtccaagctgtcatgggccagtttgagggcactgacaccctggtgaag
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                                                             ATGGACATCGTCTTCCTGATTGACGGCTCTGGAAGCATTGACCAAAATGACTTTAACCAG
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cker Drive, 6300 Sear Tower
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Pred. No. 3.1e-44;
0; Mismatches 13
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Query Match Best Local Similarity

7.3%; 72.6%;

Score 241.2; Pred. No. 3.

3.1e-44;

DB 2;

Length

3726;

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US-08-482-293A-1
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US-08-482-293A-1
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                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3268
                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/173,497 FILING DATE: 23-DEC-1993 PRIOR APPLICATION DATA:
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                 FEATURE:
                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gallatin, w. michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha
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           NAME/KEY:
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                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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                                                                              TOPOLOGY:
                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/482,293A
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                                                                                                                                                                                                                                                         APPLICANT: Gallatin, W. Michael APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5837478el H. NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS: Marshall, O'Toole, Ger. ADDRESSEE: Marshall, O'Toole, Ger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 411;
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CITY: Chicago
STATE: Illinois
                                                    CLASSIFICATION:
                                                                      FILING DATE:
                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                          COUNTRY:
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233 South Wacker
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FILING DATE: 5-AUG-1
PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 5-AUG-1994

US 08/286,889

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; LOCATION:
US-08-943-363-1
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REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/:
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-0448
TELEEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3726 base pairs
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Best Local Similarity 72.6
Matches 411; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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              cggccacgggcatcctgacagtggtg 3278
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Pred. No. 3.1e-44;
0; Mismatches 13;
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; TYPE: DNA
; ORCANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(3485)
US-09-193-043-1
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CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-65
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/363,652
EARLIER APPLICATION NUMBER: 08/943,363
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
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LENGTH: 3726
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Best Local Similarity 72.6%;
Matches 411; Conservative
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NUMBER OF SEQ ID NOS: 114
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Pred. No. 3.1e-44;
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US-08-485-618-98
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                             2833
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FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NAMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallatin, W. Michael APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5728533el NUMBER OF SEQUENCES: 103
 402
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Relicurrent APPLICATION DATA:
                                                            342
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                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 60606-6402
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                ccagacagtccccgacgccacgccaggtaggtccctggcaggagctgcaggagggggttg 2892
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No. 5728533
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233 South Wacker Drive, 6300 Sear Tower
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Pred. No. 3.1e
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INFORMATION
SEQUENCE C
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                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, .....APPLICANT: Van der Vieren, Monica APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: NO. 5817515el Human OF SEQUENCES: 103
                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                  FILING DATE: 21-DEC-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             APPLICATION NUMBER: US (FILING DATE: 5-AUG-1994 PRIOR APPLICATION DATA; APPLICATION NUMBER: US (
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                            TELEPHONE: 312 - 1
                                                                                      NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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5817515
           FOR SEQ ID NO:
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                               ttgcactgatgcagtactcaaacctcctgaagatccacttcaccttcacccaattccgga 3192
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                                                               CGGCCACGGGCATCCTGACAGTGGTG
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
                                                                                                                                  N_Geneseq_032802:*

| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to
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2000US-0249215

2000US-0249216

2000US-0249216

2000US-0249264

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2000US-0249264

2000US-0249264

2000US-0249265

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2000US-0251868

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2000US-0246476.
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2000US-0246523.
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2000US-0246525.
2000US-0246525.
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2000US-0241808.
2000US-0241809.
2000US-0241826.
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2000US-0246474.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis ar treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome ID NO 24134; immune/hematopoietic
osing and/or treating 3071pp + Sequence Listing; cancers English. polypeptides and and 31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 19-MAY-2000; 07-JUN-2000;

2000US-0209467

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Disclosure;

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                                                                                                                                                                                                                                                                                                   1696
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                   Local 289;
              TGAACCCGGGAGGCAGAGGCTGTAGTGAGCCGAGATCATGCCACTGCACTCCAGCCTGGG
                                                                                                                       ggcatggtggcgtgcacttgtaatcccagctacttgggaagctgaggcaagagaatcgct
                                                                                                                                                          gcatcagagtcacattcacgtgccatcaaaaatcaggcttggcttggctggtgcggtggctcat
                                                                    tgaacccaggagacggaagttgcagtgagctgagatcgtgccgttgcactccagcctcag
                                                                                                                                                                                                                                                                     GCAACACAGTAAGACCCCCATCTCTAAAAATATAAAATATGGCCGGGGGCAGTGGCTCAT
                                                                                                       GGCATGGTGGCATGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCT
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Pred.
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3.7e-39;
nes 70;
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RESULT 3
AAK70270/c
ID AAK702
XX AAK702
XX Human
DT 06-NOV
XX Human;
KW Cytost
XX UO2001
XX WO2001
XX Homo s
XX Homo s
Y WO2001
XX Homo s
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                                                                                                                                                                                                                                                                                                                                                                                         cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                            immune;
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                     2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-019076.
2000US-0198123.
2000US-0205515.
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                                                                                                                                                                                                                                                                                                                                                                                         metastasis;
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SEQ antigen;

IJ

NO:25082

cancer

2000US-0214886.
2000US-0215647
2000US-0215647
2000US-0215680.
2000US-0217487
2000US-0218290.
2000US-0229513.
2000US-0225114.
2000US-0225214.
2000US-0225214.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225447.
2000US-022547.
2000US-022547.
2000US-022547.
2000US-022547.
2000US-0225757.
2000US-0225759.
2000US-0225847.
2000US-0225847.

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17-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000

17-NOV-2000

01-DEC-2000

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05-DEC-2000

05-DEC-2000

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06-DEC-2000

08-DEC-2000

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08-NOV-2000

01-NOV-2000

01-NO
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I amino acid sequences given in AAM82170 to AAM91921. (I) have cytostati activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                             Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                             Disclosure;
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2000US-0241899
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2000US-0251089
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2000US-0254097.
2001US-0259678.
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                                                                                                                             ID NO
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                                                                                                                             English.
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                                                                        antigen (I)
cytostatic
     decreased
                                       and
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2000US-0229344. 2000US-0229345. 2000US-0229509. 2000US-0229513. 2000US-0230437. 2000US-0230438. 2000US-0231242.

14-AUG-2000
14-AUG-2000
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14-AUG-2000
22-AUG-2000
22-AUG-2000
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2000US-0239937

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RESULT 4
AAK78813;
ID AAK78813;
XX AAK78813;
XX AAK78813;
XX D7 07-NOV-20(
XX Human; imm
XX Human; imm
XX Human; imm
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Best Local Similarity
Matches 289; Conserv
              31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
12-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                immune; haematopoietic; immune/haematopoietic
atic; gene therapy; vaccine; metastasis; ds.
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              2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0180776.
2000US-019076.
2000US-0198123.
2000US-0205515.
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80.5%;
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Pred. No. 3.
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3.7e-39;
nes 70;
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21-SEP-2000;
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27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
20-OCT-2000;
13-OCT-2000;
13-OCT-2000;
21-OCT-2000;
21-OCT-2000;
21-OCT-2000;
21-OCT-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
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14-SEP-2000;
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12-SEP-2000;
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14-SEP-2000;
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08-SEP-2000;
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06-SEP-2000;
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14-AUG-2000;
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2000US-0233065.
2000US-0234223.
2000US-0234274.
2000US-0234997.
2000US-0234998.
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2000US-0232397.
2000US-0232398.
2000US-0232399.
2000US-0232400.
2000US-0232401.
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2000US-0231242.
2000US-0231243.
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2000US-0229344.
2000US-0229345.
2000US-0229509.
2000US-0229513.
2000US-0230437.
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2000US-0226868.
2000US-0227182.
2000US-0227009.
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2000US-0225757.
2000US-0225758.
2000US-0225759.
2000US-0226279.
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2000US-0235834
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2000US-0232081
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20-OCT 2000

01-NOV 2000

08-NOV 2000

11-NOV 2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                    Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000;
17-NOV-2000;
                                                                                         Disclosure;
                                                                                                                                                                                                                                  (HUMA-) HUMAN
                                                                                                                                                                              2001-483426/52.
                                                                                                                                                                                                          CA,
                                                                                                                                                                                                        Barash
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2000US-0250160.

2000US-0250391.

2000US-0251030.

2000US-0251988.

2000US-0251988.

2000US-0251479.

2000US-0251479.

2000US-0251868.
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2000US-0241786.
2000US-02411809.
2000US-02418109.
2000US-0244617.
2000US-0246474.
2000US-0246476.
2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246524.
2000US-0246524.
2000US-0246524.
2000US-0246526.
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2000US-0246513.
2000US-0246610.
2000US-0249216.
2000US-0249217.
2000US-0249217.
2000US-0249218.
2000US-0249296.
2000US-0249296.
2000US-0249296.
2000US-0249297.
2000US-0249297.
2000US-0249297.
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                                                                                         ID NO
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                                                                                        33625;
                                                                                                                                 human immune/hematopoietic diagnosing and/or treating
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                                                                                        3071pp + Sequence
                                                                                        Listing; English.
                                                                                                                                  cancers
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and

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RESULT
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ID AAL0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK9492 to AAK990 and AAM82169
              31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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                                                                                                              17-JAN-2001;
                                                                                                                                        02-AUG-2001
                                                                                                                                                                    WO200155320-A2
                                                                                                                                                                                                                     Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                           21-NOV-2001
                                                                                                                                                                                                                                                                                                                                               AAL05811 standard;
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                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                             Human reproductive system related antigen DNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289;
2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-01806350.
2000US-018974.
2000US-0198123.
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                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                              2001WO-US01339
                                                                                                                                                                                                                                                                                                                                               DNA;
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Pred. No. 3.
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20-OCT 2000;
20-OC
The present invention provides the protein and coding sequences o number of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoprotein of the invention.
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                                                                                                                                                                             WPI;
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                                                                                                                                                                           2001-465570/50.
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                                                                                                                           inucleic acid in preventing,
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2000US-0241786.
2000US-0241786.
2000US-0241809.
2000US-0241809.
2000US-02461809.
2000US-0246474.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246478.
2000US-0246528.
2000US-0246528.
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2000US-0246528.
2000US-0246528.
2000US-0246610.
2000US-0246611.
2000US-0246611.
2000US-0249207.
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2000US-0251188.
2000US-0251188.
2000US-0251188.
2000US-0251198.
2000US-0251199.
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                                                                                                                           molecule encoding a reproductive system antigen , treating or ameliorating a medical condition
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                                                                                            Listing;
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119-MAY -2000
28-JUN -2000
28-JUN -2000
28-JUN -2000
07-JUL -2000
07-JUL -2000
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11-JUL -2000
14-AUG -2000
14-SEP -2000
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2000US -0205515 2000US -0216887 2000US -0216887 2000US -0216887 2000US -0216887 2000US -0217487 2000US -0217487 2000US -0218290 2000US -0225513 2000US -0225213 2000US -022526 2000US -022526 2000US -022526 2000US -022527 2000US -022934 2000US -022934 2000US -023934 2000US -023934 2000US -023124 2000US -0231413 2000US -0231414 2000US -0231413 2000US -0231414 2000US -0231414 2000US -0231414 2000US -0231413 2000US -0231414 2000US -023

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RESULT 6
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ID AAK85276;
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AK85276;
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DT 07-NOV-2001 (first of the content of the content
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Best Local Similarity 81.4%;
Matches 285; Conservative
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cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0179065
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2000US-021964
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2000US-021964
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2000US-021964
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14-AUG-2000;
14-AUG-2000;
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2000US-0226688
2000US-0226688
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amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic carcivity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic antigen genomic
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01-DEC-2000
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08-NOV-2000
                                                                                                                                                                                                                                                     useful for metastasis
  sequences
                                                                                                                                                                                AAK54951 to AAK64702 encode the human immune/haematopoietic antigen amino acid sequences given in AAM82170 to AAM91921. (I) have cytosta
                                                                                                                                                                                                                                                                                                                                  Rosen
                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                               Nucleic
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  from
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2000US-0249217.
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2000US-0249244.
2000US-0249245.
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2000US-0249265.
2000US-0249265.
2000US-0249297.
2000US-0249297.
2000US-0249300.
2000US-0250160.
2000US-0251198.
2000US-02511856.
2000US-0251869.
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 invention.
immune/haematopoietic antigen
invention. AAK54942 to AAK54950
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AAK54950
                                                                                                                                                                                etic antigen (I)
have cytostatic
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and
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and

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RESULT 7
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31-TAN-2000;
04-FEB-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
11-JUN-2000;
11-JUN-2000;
11-JUN-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                            Human; respiratory antigen; respiratory disorder; throat lung disorder; nose disorder; lung cancer; gene therapy; anti allergic; anti asthmatic; anti inflammatory; olfactor respiratory active; ds.
                                                                                                                                                        17-JAN-2001;
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2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-018874.
2000US-0198174.
2000US-0198123.
2000US-0198123.
2000US-0205515.
2000US-0205467.
2000US-0215647.
2000US-0215647.
2000US-0216840.
2000US-0217486.
2000US-0217487.
2000US-0217487.
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The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens.
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117-NOV-2000
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26-JUL-2000
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2000US-022954 2000US-0224518 2000US-0224518 2000US-0225266 2000US-0225266 2000US-0225776 2000US-0225775 2000US-02257575 2000US-02257575 2000US-02257666 2000US-02256677 2000US-02256677 2000US-0225666 2000US-0225666 2000US-0225666 2000US-0225666 2000US-0225666 2000US-0225666 2000US-0225666 2000US-0225666 2000US-0225934 2000US-0225934 2000US-0225934 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-0233043 2000US-0233043 2000US-0233043 2000US-0233063 2000US-0233063 2000US-0233497 2000US-0234997 2000US-0234997 2000US-0235366 2000US-02341785 2000US-0241785 2000US-0241808 2000US-0241809 2000US-02441809 2000US-0244617 2000US-0244617 2000US-0244617

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RESULT AAS36168 ID AAS3 AC AAS3 AC AAS3 AC AAS3 XX DT 17-D XX Card KW Chic KW Chic KW Copht KW Copht KW Gobt K
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Matches 270
        31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                   Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; gastrointestinal disorder; renal disorder; respiratory disorder; skin aging; organ transplantation; tissue regeneration;
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at ftp.wipo.int/pub/published_pct_sequences.
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70; Conservative
    2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-018350.
2000US-018974.
2000US-0199076.
2000US-0199123.
2000US-0199123.
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86.8%;
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01-DEC-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
useful in
disorders
          Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of
                                                                                                           New cardiovascular system relate
useful for diagnosing, treating
cardiovascular system -
                                                                                  Claim
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CC Note: The sequence data for this patent did not form part of the printed content of the prin
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Matches
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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                                                                                                         17-JAN-2001;
                                                                                                                                                                                            WO200157182-A2
                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                               cytostatic;
                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK79698 standard;
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                                                                                                                                                                                                                                                                                                                                              immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                     immune;
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Similarity 87.6%;
68; Conservative
; 2000US-0179065.
; 2000US-0180628.
; 2000US-0184664.
; 2000US-0186350.
                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                         2001WO-US01354
                                                                                                                                                                                                                                                                                                     haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                 therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 6154
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01-NO
                                                        Nucleic acids encoding useful for preventing, metastasis -
                             Disclosure;
    AAK54951
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the human immune/haematopoietic antigen
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                            Sequence
                            Listing; English.
                                                                       antigen
                                                                       polypeptides, and
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2000US-022528.
2000US-022934.
2000US-023124.

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CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK64990 and AAM82169 CC especial special s
Sequence 6154 BP; 1629 A; 1274 C; 1369 G; 1382 T; 500 other;
                                                                                                                                                                                                                        sequences used in the exemplification of the present invention
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рь ρ 밁 ρy 밁 γQ 밁 δ. δÃ Š В 밁 ρy Query Match Best Local Best Local Similarity 39.1 Matches 747; Conservative 1166 1106 1046 441 142 501 381 321 986 926 866 262 ggctggatgtggtggctcacgcctgtaatcccagtactttgggaggaggaggaggtgggagga gctgaggtgggagaattgcttgagtctgggaatttgaggctgcagtgagccotgatcatg aaaaacaaaaaattagctgggcatggtgtgtgtatcagtaatcccagtgact-gggag ttgcttgagtccaggagctcgagaccagcatgggcaacatagtgcgatctcytctctaca 261 tctgccccaccatagacaaccactcttctgatttctatcttcgtagatgaatttgccca gctgaggcaagagaattgcctgaacctgggaggcagaggttacagtgaaccaagatcgca aaaaatacaaaaattagctgggcgtggtggcgtgcgcctgtaattccagctactcgggag tcacttgaggtcaggagtttcagaccagcctggccaacatagcgaaaccttytctctact ggctgggtgcgtggctcaggcctgtaatcccagcactttggaaggccgaggcaggagga ttctcttgtatatgaaaggaaccagacatt-aggcattctggtgtctggtttctttcact ggtccatgagggaacctcccagccagcgaaggctgtagggatgagccagactagggaggt 7.4%; Score 244.8; DB 22; Pred. No. 7.1e-39; 1; Mismatches 1068; Indels Length 6154 75; Gaps 1105 1225 1165 1045 559 500 440 380 320 985 925 201 9;

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Best Local Similarity
Matches 275; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis .
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                                                                                                         aaccccatctttaccaaaaatataaaaattagccgggcatggtggcgtgcacttgtaatc
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84.4%;
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0; Mismatches
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Barash SC, Ruben SM:

2001-483426/52.

Nucleic aci useful for metastasis acids encoding for preventing, sis human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and

Disclosure; SEQ ID ö 30980; 3071pp + Sequence Listing; English

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM8170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to it is complement the patients own production of (I). Additionally, (I) CC expression by rectifying mutations of (I). Additionally, (I) CC concers and caids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic artigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM62169 CC represent sequences used in the exemplification of the present invention.

Sequence 25541 BP; 7495 A; 5717 C; 5419 G; 6910 T; 0 other;

Similarity

7.4%;

22;

Length 25541;

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99ctgggtgcggtggctcatgcttataatcccagcactttgggaggccgagatgggcgta
                                                             tcccctgaggtcaggagtttgtgaccagcctggccaacatggtgaaaccccatctttacc 1855
                                                                                                 99cc999cgc9gtggctcacgcctataatcccagcactttaggaggctgaggcgggtgga 16645
                                                                                                                                    Conservative
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Pred. No. 1.4e-38;
0; Mismatches 42
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tandard; DNA; 32248 BP. 1 (first entry) quence #208 encoding for novel human respiratory antigen. piratory antigen; respiratory disorder; throat disorder; qir; anti asthmatic; lung cancer; gene therapy; cytostatic; y active; ds. 1. 1. 2001WO-US01333. 1; 2001WO-US01333. 1; 2000US-0184664. 2000US-0184664. 2000US-0184667. 2000US-0198123. 2000US-0198123. 2000US-025515. 2000US-025515. 2000US-025516. 2000US-025516. 2000US-025526. 2000US-025526. 2000US-025526. 2000US-0255278. 2000US-025579. 2000US-025579. 2000US-025588. 2000US-025579. 2000US-025588. 2000US-025579. 2000US-025588. 2000US-025579. 2000US-025579. 2000US-025588. 2000US-025579. 2000US-025579. 2000US-025579. 2000US-025579. 2000US-025579. 2000US-025588. 2000US-025579. 2000US-02579.	ccyttycactocaycotcaycaacayayoyayactocatotcaaaaaaaaaa
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CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

polypeptides, and

Disclosure; SEQ ID NO 30984; 3071pp + Sequence Listing; English

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC antino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC polynucleotides may be used to produce the secreted (I), by inserting CC protein. (I) proteins and polynucleotides may be used to prevent. CC diagnose and treat immune/haematopoietic related diseases, especially CC cancers and cancer metastases of haematopoietic derived cells. AAK64703 CC sequences from the present human immune/haematopoietic antigen genomic compresent sequences used in the exemplification of the present invention.

Sequence 34435 BP; 10095 A; 7731 C; 7309 G; 9300 T; 0 other;

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2000US-0229344. 2000US-0229345. 2000US-0229509.	; 2000US-0228924. ; 2000US-0229287. ; 2000US-0229343.	2000US-0227009.	; 2000US-0226279. ; 2000US-0226681.	; 2000US-0225758. ; 2000US-0225759.	; 2000US-0225447. ; 2000US-0225757.	; 2000US-0225270.	; 2000US-0225267.	; 2000US-0225214. ; 2000US-0225266	; 2000US-0224519. ; 2000US-0225213.	; 2000US-0224518.	2000US-0220963.	; 2000US-0217496. ; 2000US-0218290.	; 2000US-0217487.	200008-0216647.	; 2000US-0214886.	; 2000US-0209467.	2000US-0198123.	; 2000US-0189874.		; 20000S-0179065.	COCTMO-ORD	200100 - 120135		-A2.	19 .	gene therapy; vaccine; metastasis; ds.	De Promotoriotion immisso (bronnette)	e/haematopoietic antigen genomic sequence SEO	(first entry)		tandard; DNA; 15914 BP.				1888 a 2046	ccactgcactccagcctgggcaacagagccagactccttctcaagaaaaaaaa	cgttgcactccagcctcagcaacagagcgagactccatctcaaaaaaaa	gctgaggcaggagaattgcttgaacccgggaggaggaggttgcagtgagctgagatcgta
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                                                                                                                                                                                                                                                                                                                                        proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK94550 and AAM92169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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agctacttgggaagctgaggcaagagaatcgcttgaacccaggagacggaagttgcagtg
                                                                                                           cgagatgggcgtatcccctgaggtcaggagtttgtgaccagcctggccaacatggtgaaa 1842
                                               ccccatctttaccaaaaatataaaaattagccgggcatggtggcgtgcacttgtaatccc
                                                                                                                                                         AAACATGCCACAGGGCTGGGCGCGGTTGGTTCATGCCTGTAATCCCAGCACTTTGGGAAGGC 3664
                                                                                             CGAGGTGAGTGGATCACCTGACGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAA
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82.1%;
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Pred. No. 1.6e
0; Mismatches
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11-JUL-2000;
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                                                                            14 - AUG -
14 - AUG -
                                                                                                                                                                                                                                                                                                                                                                                     Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ds.
                                                                                            14 - AUG -
14 - AUG -
                                                                                                                                                           26-JUL-
14-AUG-
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25423 BP; 5518 A; 6899 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen
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                        tgaacccaggagacggaagttgcagtgagctgagatcgtgccgttgcactccagcctcag
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Search completed: September 27, 2002, 15:09:38 Job time: 10015 sec

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Noti,J.D., Johnson,A.K. and Dillon,J.
Direct Submission
Submitted (16-SEP-1999) Molecular Biology, Guthrie Research
Institute, One Guthrie Square, Sayre, PA 18840, USA Noti,J.D., Johnson,A.K. and Dillon,J.D. Structural and functional characterization of the leukocyte integrin gene CDIId. Essential role of Sp1 and Sp3 J. Biol. Chem. 275 (12), 8959-8969 (2000) 20187620 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 11557) Homo sapiens 10722744 Q, DNA linear PRI 06-APR-2000 gene, promoter and partial cds.

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Description

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21 GACATCACCTCCCTGGGCCTNNNNNTTCCCCCAA
1 CTCCCCAGCCTCCCCCGGGAGTGGAAGGCCA
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01 tatgttgtcccaggcttccctgctcccactcatg
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901 ccattctgcttcctgtccttccactcctgtggga
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781 attattttgggtgtccattctcctctggaggggctct;
721 ggcatotgatokgtagtttgatottatttottg
661 tcgaactgttggcctcaagcaatccacctgcca

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Sequencing of Human Chromosome
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quality: 147299 bases at least Q40 quality: 157879 bases at least Q30 quality: 159986 bases at least Q20 insert size: 163000; agarose-fp esinsert size: 167296; sum-of-contig:
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Primates;
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                                      ATTTATCTTCTCCCCAACCCCATGTAATAAATATTAAAATATTGTGTTAAATGCTAAATT
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**NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

** This record will be updated with the finished sequence
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160316		Db 16025	
1020 160256	61 gtaccaactggctcctgaggcctggggggggggtggtcttctggggagaaggaag	Qy 96 Db 16019	
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160196		Db 16013	
900	41 ctageteccettetecetgectetetgeaggeteacatecaeatgecaagaeetetgeag	Oy 84	
160136		Db 16007	
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780	21 ggcatctgatckgtagtttgatcttatttcttgctgagtagtagtagcccatggcatgacttt	Qy 72	
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660 159896	01 cagtttgttctttgttatttattgtaaagacagggtctggctatgttgcctaggctggtc	Qy 60 Db 15983	
600 159836	41 gtgtctggtttctttcacttaagataaaattgagttaacctgtattgttgtacagaactg 	Qy 54	
540	81 togtagatgaattttgcccattctcttgtatatgaaaggaaccagacattaggcattctg	Qy 48	
159776		Db 15971	
480 159716	21 aaaaaaaaaagtttcctctctcccccaccatagaccactcttcttgtgatttctatct	Qy 42 Db 15969	
420 159656	61 tgcagtgagccctgatcattgccactgcattccagcattggcgacatagcaaaacttgtca 	Qy 36	
360	01 gtaatcccagtgactgggaggctgaggtgggagaattgcttgagtctggggaatttgaggc	Qy 3(
159596		Db 1595)	
300	41 tagtgcgatctcgtctctacaaaaaacaaaaaattagctgggcatggtggtgtgcatca	Qy 24	
159536		Db 15947	
240	81 tgggaggaggaggtgggaggattgcttgagtccaggagctcgagaccagcatgggcaaca	Qy 11	
159476		Db 1594;	

RESULT AC026471/ LOCUS DEFINITIO	Qy 2221 Db 161454	Qy 2161 Db 161394	Qy 2101 Db 161334	Qy 2041 Db 161274	Qy 1981 Db 161214	Qy 1921 Db 161154	Qy 1861 Db 161094	ОУ 1801 Db 161034	Oy 1741 Db 160974	Qy 1681 Db 160914	Qy 1621 Db 160857	Qy 1561 Db 160797	Qy 1501 Db 160737	Qy 1441 Db 160677	Qy 1381 Db 160617	Qy 1321 Db 160557	Qy 1261 Db 160497
3 C AC026471 189467 bp DNA linear HTG 19-S N Homo sapiens chromosome 16 clone RP11-452L6, WORKING DRAFT	gatotoggtaggcocococococococococytycocococococococtcotyt 2273	gagcctacgatcttccaggaggatgcaggcgtggtttgggcagagcgtggtgcagttcggt 2	ccgcccaccaatattcctcagtcctggcttcttatcatggattcaacctggatgtggag 2	aaaagaggctgggaggtcctagggattggggcttctttaactcccagcctcc 	. gcactccagcctcagcaacagagcgagactccatctcaaaaaaaa	ggcaagagaatcgcttgaacccaggagacggaagttgcagtgagctgagatcgtgccgtt	tataaaaattagccgggcatggtggcgtgcacttgtaatcccagctacttgggaagctga	. tgaggtcaggagtttgtgaccagcctggccaacatggtgaaaccccatctttaccaaaaa 	ggtgcggtggctcatgcttataatcccagcactttgggaggccgagatgggcgtatcccc 	cccctgctgaaaactgcatcagagtcacattcacgtgccatcaaaaatcaggcttggctg	gacatcacctcctgggcctnnnnnttcccccaagtcctgactgcacgtagggaagaggc	Ctccccagcctcccccgggagtggaaggccacagaagccaccagggaggg	. tatgttgtcccaggcttccctgctcccactcatggagtccctggtgtgggtgacagaggt	gaatgaagagggctcaggggctgtgctcaggtggcgactaagctacctctccagctggc	. ggagctgaggcaggggagtgcttcatgtgcgagtggcccggagtcagtagagtgtgacct 	. ggggactccatctqggagggcaggctggggggctggtggtcggctccaaccatcttatga	. tgcttcttctgagtggtaagtggggccagggtgctggggagaagcttggaggagttctga
SEP-2001		2220 161453	2160 161393	2100 161333	2040 161273	1980 161213	1920 161153	1860 161093	1800 161033	1740 160973	1680 160913	1620 160856	1560 160796	1500 160736	1440 160676	1380 160616	1320 160556

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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 106708: contig of 106708 bp in length

* 106809 106808: gap of unknown length

* 108237 108336: contig of 1277 bp in length

* 108237 108336: gap of unknown length

* 108337 169713: contig of 61377 bp in length

* 169814 175319: contig of 61377 bp in length

* 169814 175319: contig of 5506 bp in length

* 175320 175419: gap of unknown length

* 175420 189467: contig of 14048 bp in length.
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 189467)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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/db_xref="taxon:9606"
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1. .189467
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                                     gagcctacgatcttccaggaggatgcaggcggctttgggcagagcgttggtgcagttcggt
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* consists of 20 contigs. Gaps between the contigs
* are represented as runs of N. The order of the places
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 46156 46612: gap of unknown length
* 46156 46612: gap of unknown length
* 48053 49874: contig of 983 bp in length
* 48053 49874: contig of 1822 bp in length
* 49875 50331: gap of unknown length
* 50332 52542: contig of 2211 bp in length
* 53300 53239: contig of 2711 bp in length
* 53657 63110: contig of 400 bp in length
* 53657 63110: can of unknown length
* 63657 63110: can of unknown length
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Homo sapiens chromosome 16q24.3
SEQUENCE, 20 ordered pieces.
AC074302
AC074302.1 GI:9454507
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-JUL-2000) Cytogenetics & Molecular Genetics, Women's & Children's Hospital / Bionomics, 28 Dalgleish Street Thebarton, Adelaide, South Australia 5031, Australia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Website:http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html
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4: gap of unknown length
7: contig of 1081 bp in length
7: contig of 1416 bp in length
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3: gap of unknown length
3: contig of 5740 bp in length
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                                                                                                                                                                                       This clone is from the human chromosome 22-specific cosmid library LL22NCO3, constructed at the Biomedical Sciences Division, Lawrence Livermore National Laboratory, Livermore CA 94550, under the auspices of the National Laboratory Gene Library Project sponsored by the U.S. Department of Energy. The source of the flow sorted chromosomes was a human/hamster hybrid containing chromosomes Y, 22 and 9. This clone is part of a cosmid conting isolated using YACs from the Sanger Centre chromosome 2 YAC conting described by
                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
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Submitted (03-FEB-1999) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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Submitted (04-OCT-1996)
4 (bases 1 to 38468)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                     SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mailto:sapiens@watson.wustl.edu
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                                                                                                                                                                      et al., Nature 377 Suppl.,
                                                                                                                                     Location/Qualifiers
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/clone_lib="LL22NC03"
1. .285
                                                   /map="22q12"
                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
                                /clone="N73F4"
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906. 988
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Consensus quality: 112209 bases at least Q40
Consensus quality: 125309 bases at least Q30
Consensus quality: 127423 bases at least Q30
Consensus quality: 127423 bases at least Q20
Estimated insert size: 77960; agarose-fp estimation
Estimated insert size: 135335; sum-of-contigs estimation
Quality coverage: 5.86 in Q20 bases; agarose-fp estimation
Quality coverage: 3.37 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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Homo sapiens chromosome 5 clone
SEQUENCE, 34 unordered pieces.
AC093222
                                                                                                                                                                                                                                                     Direct Submission
Submitted (16-AUG-2001) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
                                                                                                                                                               Project Information
Center Project Name: 707152
Center clone name: CITB-H1_2207E19
                                                                                                                                                                                                                      Center: Joint Genome Institute
Center Code: JGI
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1 (bases 1 to 138635)
DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS
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                                                                                                                                                                                                            Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                          DOE
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84.5%;
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Primates;
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Summary Statistics
Consensus quality: 93209 bases at least Q40
Consensus quality: 114842 bases at least Q30
Consensus quality: 124351 bases at least Q20
Estimated insert size: 50000; pulse field gel
Estimated insert size: 143546; sum-of-contigs
                                                                                                                                                                                   Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gl:7709284.
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 148846)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 54 unordered pieces. AC008714
                                                                                                                  Center Project Name: 95978, H336
Center clone name: CIT978SKB_82L22
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Quality coverage: 6.24 in Q20 bases; pulse field gel estimation Quality coverage: 2.17 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces to consist of 54 contigs. The true order of the pieces to consist of 54 contigs. The true order of the pieces to consist of 54 contigs. The true order of the pieces to consist of 54 contigs. The true order of the pieces to consist of 54 contigs. The true order of the pieces to consist of 54 contigs. The true order of the pieces to consist of 54 contigs. The true order of the pieces to consist of 54 contigs.
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                                                                                                                                                                                                                                                                                                                                   Consensus quality: 137047 bases at least Q40
Consensus quality: 148952 bases at least Q30
Consensus quality: 152398 bases at least Q30
Estimated insert size: 150000; pulse field gel estimation
Estimated insert size: 157126; sum-of-contigs estimation
Quality coverage: 6.32 in Q20 bases; pulse field gel estimation
Quality coverage: 6.43 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-0CT 1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USI
On Jun 21, 2000 this sequence version replaced gi:7710596.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summary Statistics
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Homo sapiens chromosome 5 clone
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                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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 3 (bases 1 to 209197) Waterston, R.H. Direct Submission
                                          Mead,K., Ryan,E., Lamar,B., I
The sequence of Homo sapiens
Unpublished (2001)
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Sulston, J.E. and Waterston, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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3142: contig of 6316 bp in length
31522: gap of unknown length
41015: contig of 9493 bp in length
41115: gap of unknown length
57707: contig of 16592 bp in length
57807: gap of unknown length
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Submitted (09-MA-2002) Department of
University, 4444 Forest Park Avenue, S
On Sep 19, 2001 this sequence version
                                                                                                                                                                                                                                                 Direct Submission
Submitted (19-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 209197)
                                                                                                                                                                                                                                    Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-APR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Center project name: H_NH0418H16
                   Contact: sapiens@watson.wustl.edu
                                                                                    Center: Washington University Genome Center code: WUGSC
                                                               Web site: http://genome.wustl.edu/gsc
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                                                                                                                                                                   )9-JAN-2002) Department of Genetics, 4444 Forest Park Avenue, St. Louis,
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Missouri 6
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P. I., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

The sequence from 130000 bp to 131200 bp can not be guaranteed due to a GC rich tandem repeat. There are approximately 1400 bases of this tandem missing according to the restriction digest and PCR.

The clone sequenced to the left is RP11-568D19; the clone sequenced to the right is RP11-340F16, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-418H16; actual end is at base position 209197 of RP11-418H16.

NEIGHBORING SEQUENCE INFORMATION:

ata from ACO21014 was used to finish ACO07389

уd

RP11-418H16 from base position 32235 to 32244 is represented sequence derived from PCR.

RES Location/Qualifiers
1. 209197
Source Jorganism="Homo sapiens"
/dryanism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"

FEATURES

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      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.8%; Score 257.2; DB 9; Best Local Similarity 81.4%; Pred. No. 8.2e-50; Matches 298; Conservative 0; Mismatches 68;
                                                                                                                                                                                                                                                        47270 GCTGGGATTTGAATCCCAAAACTTTTGTCTTGTCATAAAAAAGACAAACTTGGCCAGGTGC 47329
                                                                                                        47630 GACAAA 47635
                                                                                                                                                                                                                                                                                                                                                              47330
                                                                                                                                                                                                          47510 GAGAATCGCATGAACCCAGGAGGCGGAGGTTGCAGTGAGCTGAGATCTCACCACTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                            1686 gctgaaaactgcatcagagtcacattcacgtgccatcaaaaatcaggcttggctgggtgc 1745
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                                                                                                                                                                                                                                                                                                                                                           gagaatcgcttgaacccaggagacggaagttgcagtgagctgagatcgtgccgttgcact 1985
                                                                                                                                                        166372 bp DNA linear PR: Human DNA sequence from clone RP11-336N8 on chromosome 9q21.11-21.31, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16364. .16473
/rpt_family="Alu"
16474. .16781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
12118. .12141
/note="similar to Homo s
(NID:g12687098)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="ERV1" 16364. .16473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="Alu"
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15351. .15643
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4. .12763
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                                          PRI 30-JAN-2002
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AUTHORS
TITLE
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Best Local
                                                                                1778 gaggccgagatgggcgtatcccctgaggtcaggagtttgtgaccagcctggccaacatgg 1837
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                                     1838
                                                                                                                                                                                                                      1718 ccatcaaaaatcaggcttggctgggtgggctcatgcttataatcccagcactttgg 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                       CCTTAAAAAATGAAGACAGGCCGGGCGCGCGCTGGCTCATGCCTGTAATCCCAGCACTTTGG 111782
tgaaaccccatctttaccaaaaatataaaaaattagccgggcatggtggcgtgcacttgta 1897
                                                                                                                                                                                                                                                                                                                  286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: RMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery(sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:17154270. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                         Similarity 85.3
86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group. Further information can be found at http://www.sanger.ac.uk/HGP/chr9
RP11-336N8 is from the library RPCI-11.2 constructed by the of Pleter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the overlapping clone, as we submit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babbage, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Sequence from clone PCR only."
105432. .105570
/note="Sequence from overlapping clone RP11-83016
(AL353594). Assembly confirmed by restriction digest."
1 32616 c 33334 g 49632 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11.2"
57469. .57517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="q21.11-21.31"
/clone="RP11-336N8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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85.1%;
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                                                                                                                                                                                                                                                                                                      Score 256; DB 9; I
Pred. No. 1.6e-49;
Pred. No. 1.6e-49;
                                                                                                                                                                                                                                                                                                                                                             Length 166372;
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                                                                                  111722
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FEATURES

/chromosome="22"

/clone="RP1-67C13"

/organism="Homo sapiens" /db_xref="taxon:9606" Location/Qualifiers

.56913

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REFERENCE
AUTHORS
TITLE
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ORGANISM
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On Dec 13, 1999 this sequence version replaced gi:1617078.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'; The fellowing abbroads and the sequence all sequence the sequence is ambiguous, there is an annotation using the 'unsure';
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atcccagctacttgggaagctgaggcaagagaatcgcttgaacccaggagacggaagttg
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between neighbouring submissions.
The true left end of clone RP1-67Cl3 is at 1 in true left end of clone CITF22-111A3 is at 56810
                                                                                            IMPORTANT: This sequence is not the entire insert of clone RP1-67C13 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap
                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr22
RPI-67C13 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For furthe
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HM367C13 56913 bp DNA Human DNA sequence from clone RP1-67C13 an exon of the gene for a novel protein ESTs, STSs and GSS, complete sequence.
                                                                                                                                                                                                    VECTOR: PCYPAC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="17 copies 2 mer a
4257. .4376
/note="2 ^^^'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4359. .4396
/note="19 copies 2 mer at 84 conserved"
4383. .4502
/note="2 copies 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                    ,....te="16 copies 2 mer ac 5416. .5527 ,note="2 com:
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'note="17 coniar"
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                                                                                                                                                                                                                                                                                                                         /note="Alux repeat: matches 1.
complement(8343. .8794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(246.
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/note="match: STS: Em:AL022556; match: STS: Em:HS67C13S"
                                                                                                                                                                                                              'note="match: GSS: Em:AQ053906"
                                                                                                                                                                                                                                 complement(9103.
                                                                                                                                                                                                                                                                                                                                                              977. .7683
/note="L1MB7 repeat: matches 5398. .6136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="TIGGER1 repeat: matches 8. .157 cf consensus"
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3198. .3373
note="Looper repeat: matches 1049. .1231 of consensus"
                                                3368. .13785
note="L2 repeat: matches 1752.
                                                                                 note="match: STS:
                                                                                                               note="match: STS: Em:G49328"
                                                                                                                                                 'note="match: GSS: Em:B14175"
                                                                                                                                                                               note="MIR repeat: matches 67.
                                                                                                                                                                                                                                            note="MIR repeat: matches 46.
                                                                                                                                                                                                                                                                              'note="match: GSS: Em:AQ105099"
                                                                                                                                                                                                                                                                                                             note="match: GSS: Em:B95656"
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1976. .4095
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971. .2277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Tigger3b repeat: matches 1.
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3. .4742
te="2 copies 60 mer 90 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                           .6031
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.3979
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                                                                                                                                  .10880
   MIR repeat: matches 81.
16182
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                  .216 of consensus"
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/note="LlMC/D repeat: matches 25. .144 of consensus"
/note="LlMC/D repeat: matches 5341. .5439 of consensus"
/note="MIT1B repeat: matches 1. .180 of consensus"
9696. .19815
note="Allux repeat: matches 1. .180 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 1673. .1935 of consensus"
16356. .16809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(22893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2284;
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                                                                                                                                                           /note="MIR repeat: matches 119.
35185. .35437
/note="match: STS: Em:G49331"
35774. .36190
/note="%1MB6 repeat: matches 57:
                                                                                                                                                                                                                                                                                                                                                                                                         complement(30465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(16943
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35121. .35182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSq repeat: matches 1. .295 of consensus"
!4062. .24369
'note="AluY repeat: matches 6. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match: GSS: Em:AQ434057"
7180. .17418
                                                                                                                                                                                                                                                                              'note="6 copies 34 mer 96 conserved"
|1649. .31747
                                                                                                                                                                                                                                                                                                                            note="match: GSS: Em:AQ094508"
                                                                                                                                                                                                                                                                                                                                                            'note-"match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96. .26794
te="3 copies 33 mer 85 conserved"
94. .27687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               te="match: GSS: Em:AQ637472"
blement(22893. .23367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e="Aluyb8 repeat: matches 1.
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   .88;
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                                                                                                h: STS: Em:G32626"
   Score
                                                                                                                                                              repeat: matches 5730.
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5943. .17387)
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                                                                 STS:
                                                                                                                                STS:
                                   STS: Em:G49333"
                                                                                                                                                                                                                                                                                                                                                            GSS: Em: AQ478810"
                                                                                                                                                                                                                                                                                                                                                                                            GSS: Em: AQ506060"
                                                                                                                                                                                                                                                                                                                                                                                                                           GSS:
   255.8;
                                                               Em:G49332"
                                                                                                                                Em: 243443"
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   DB
   9
                                                                                                                                                                                                                                                             .114 of consensus"
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 Length 56913;
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RESULT 12
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                                                                                                                                                                                                                                                        RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boushgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Crant, G., Hagos, B., Heaford, A., Horton, L., Keratas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marguis, N., McEwan, P., McGurk, A., McKernan, X., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Kiley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Timmell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
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                                                                                                         Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 9, 2001 this sequence version replaced gi:13958517.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 182504)
Birren, B., Linton, L.,
                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-19A13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 4 clone
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                                           Center: Whitehead Institute/ MIT Center
site: http://www-seq.wi.mit.edu
                                                                       -- Genome Center
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                                                                                                                      Similarity
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1055 1154: gap of 100 bp
1155 27377: contig of 26223 bp in length
27378 27477: gap of 100 bp
27478 57319: contig of 26224 bp in length
57320 57419: gap of 100 bp
57420 108311: contig of 50892 bp in length
108312 108411: gap of 100 bp
108412 19879 of 100 bp
147520 147619: gap of 100 bp
147620 182504: contig of 39108 bp in length
147620 182504: contig of 34885 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a Tworking draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                   53748
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Center clone name: 19_A_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 8.0 in Q20 bases; Quality coverage: 7.6 in Q20 bas.
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Consensus quality: 178778 bases at least Q40
Consensus quality: 180960 bases at least Q30
Consensus quality: 181637 bases at least Q20
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Insert size: 182004; sum-of-contigs
                                                                                               Conservative
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                                                                                                                 Score 255.6; DB 2; Pred. No. 1.9e-49;
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aggccgagatgggcgtatcccctgaggtcaggagtttgtgaccagcctggccaacatggt 1838

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                                                                                                                                                                                                                                                  www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-SEP-1999) production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut 3 (bases 1 to 3792)
DOE Joint Genome Institute and Stanford Human
                                                                                                                                                                                                                                                                                                                                                        Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598 USA On Aug 30, 2001 this sequence version replaced gi:14916144. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-JUL-2001) DOE Joint of Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 37492)
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                            /clone="LLNLR-304C3"
10406 c 9521 g
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/db_xref="taxon:9606"
                                                                                                                                                                                              'chromosome="19"
                                                                           7.7%;
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              Smit, A.F.A. & Green, F. (1990-1997), http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                 Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 2, 2001 this sequence version replaced gi:8079355.
                                                                              All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                         Submitted (21-MAR-2000) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                        Direct Submission
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Unpublished
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Contact: sequence_submissions@genome.wi.mit.edu

Web site: http://www-seq.wi.mit.edu

Center code: WIBR

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Insert size: 170000; agarose-fp
Quality coverage: 8.6 in Q20 bases; agarose-fp
Quality coverage: 8.4 in Q20 bases; agarose-fp
Quality coverage: 8.4 in Q20 ba
NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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1 2053: contig of 2053 bp in length
2054 2153: gap of 100 bp
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11948 15047: gap of 100 bp
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119582 33782: contig of 14101 bp in length
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Center clone name: 815_I_9
Center clone name: 815_I_9
Sequencing vector: M13; M77815; 55% of reads
Sequencing vector: Plasmid; n/a; 44% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0,96073
Consensus quality: 189944 bases at least Q40
Consensus quality: 171067 bases at least Q30
Consensus quality: 171067 bases at least Q20
Consensus quality: 171067 bases at least Q20
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          AL Submitted (11-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 19, 1999 this sequence version replaced gi:5050947.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: KMBL; Sw., SWISSPROT; Tr., TREMBL.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from clone 215D11 on chromosome 1p36.12-36.33 Contains a gene for a RNA-binding protein regulatory subunit, a gene similar to rat gene 3, a pseudogene similar to PLA-X, ESTs, GSSs and CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 122279)
                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                        Wray,
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a 35535 c 36175 g
is ambiguous, there is an annotation
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/note="assembly_fragment
clone_end:T7
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Pred. No. 2.7e-49;
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using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/HGP/Chrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The true right end of clone 892Fl3 is at 100 in this sequence. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215D11 is from the human BAC library described in U-J. Kim et al. (1996) Genomics 34, 213-218. VECTOR: pBAC1081. IMPORTANT: This sequence is not the entire insert of clone 215D11. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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                                                                                                                                                                                                                              /note="MER84 repeat: 9586. .9691
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSx repeat: 7725. .8034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSx repeat: 7034. .7330
/evidence=not_experimental
join(10536. .10579,11607. .11719,14168.
19738. .19807,26496. .26582,33738. .341
/gene="bK215D11.1"
/note="RNA-binding protein regulatory s
                                                                                             10086. .11010
/note="CpG island"
                                                                                                                                                                                                                                                                                                                                                             note="L1MA4
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Monte="L2 repeat: matches 2600.
862. .4175
Noote="AluSq repeat: matches 1.
                                                                                                                                    'note="L2 repeat: matches
                                                                                                                                                                       note="L1MA4 repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluSx repeat: matches 3.
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'note="HAL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluSg/x repeat: matches 135.
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organism="Homo sapiens"
organism="Homo sapiens"
organism="Homo sapiens"
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                /note="Alusx repeat: matches 21601, .21899
                                                                                                                                                                                                                            complement(join(19774. .19807,26497.
/note="match: STS: Em:G22443"
                                                                                                                                                                                             /evidence=not_experimental
20495. .20806
                                                                                                                                                                                                                                                             complement(19467. .20068)
/note="match: GSS: Em:B73152.1"
/evidence=not_experimental
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/product="bK215b11.1 (RNA-binding protein regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Em:AA129779 Em:AA082613 Em:H38029 Em:AA716183 Em:AA388672 Em:AA308838 Em:D61064 Em:D53402 Em:W42607 Em:AA329174
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Em:AB015652
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//note="AluJo repeat: matches 2.
16872. 17173
/note="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15260. .15564
/note="AluJo repeat: matches 1.
15641. .16331
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AAICAGPTALLAHEIGFGSKVTTHPLAKDKMMNGGHYTYSENRVEKDGLILTSRGPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="bK215D11.1"
|join(11630. .11719,14168. .14269,18189.
|26496. .26582,33788. .33898)
|/gene="bK215D11.1"
                                                                                                                                                                                                                                                                                                                                                                                   note="AluSg1 repeat: matches 13056..13257
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12217. .12518
/note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/product="bK215D11.1 (RNA-binding protein regulatory
                                                                     'note="MADE1 repeat: matches 32.
                                                                                                                                       'note-"AluJo repeat: matches 1.
                                                                                                                                                                          'note="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                'note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                         8429. .18721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MA5A repeat: matches 5587. .6294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluJb repeat: matches 113. .308 of consensus"
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[4646. .14832
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13369. .13641
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                                                                                                      'note="Charliel repeat: matches
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                                                     21600
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repeat: matches
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Query Match 7.7%; Score 254.8; DB 9; Length 122279; Best Local Similarity 87.0%; Pred. No. 3e-49; Matches 280; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                    46604 ACTAAAAATACAAAAATTAGCTGGGCATGGTGGCGTGCACCTGTAATCCCAGCTACTAGG 46545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"AluSg/x repeat: matches 73. .309 of consensus" 26830. .27139 /note-"AluSg repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"AluSx repeat: matches 116. .298 of consensus" 2872. .23189
/note-"AluJo repeat: matches 1. .300 of consensus" 23192. .23506
/note-"AluYb8 repeat: matches 1. .316 of consensus" 23692. .23997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluY repeat: matches 1. .309 of consensus" 26302. .26427
/note="FLAM_C repeat: matches 2. .131 of consensus" 26595. .26831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSq repeat: matches 1. .307 of consensus"
25555. .25863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21904. .21985
/note="Charliel repeat: matches 2642. .2758 of consensus"
22335. .22587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSq repeat: matches 60.
22588. .22769
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Search completed: September 27, 2002, 14:20:07 Job time: 10214 sec